Claims:

1. An isolated polynucleotide, comprising a polynucleotide sequence selected from the group consisting of

   a) polynucleotide which is at least 70% identical to a polynucleotide that codes for a polypeptide which comprises the amino acid sequence of SEQ ID No. 2,

   b) polynucleotide which codes for a polypeptide that comprises an amino acid sequence which is at least 70% identical to the amino acid sequence of SEQ ID No. 2,

   c) polynucleotide which is complementary to the polynucleotides of a) or b), and

   d) polynucleotide comprising at least 15 successive nucleotides of the polynucleotide sequence of a), b) or c).

2. The polynucleotide as claimed in claim 1, which is capable of replication in coryneform bacteria.

3. The polynucleotide as claimed in claim 1, wherein the polynucleotide is an RNA.

4. The polynucleotide as claimed in claim 2, comprising the nucleic acid sequence as shown in SEQ ID No. 1.

5. The DNA as claimed in claim 2 which is capable of replication, comprising

   (i) the nucleotide sequence shown in SEQ ID No. 1, or

   (ii) at least one sequence which corresponds to sequence (i) within the range of the degeneration of the genetic code, or

   (iii) at least one sequence which hybridizes with the sequence complementary to sequence (i) or (ii), and optionally

(iv) sense mutations of neutral function in (i).

6. The polynucleotide sequence as claimed in claim 2, which codes for a polypeptide which comprises the amino acid sequence in SEQ ID No. 2.

7. A coryneform bacterium in which the metF gene is enhanced.

8. A coryneform bacterium serving as a host cell, that contains a vector which carries a polynucleotide as claimed in claim 1.

9. A process for the fermentative preparation of L-amino acids, comprising:

a) fermentation of the coryneform bacteria which produce the desired L-amino acid and in which at least the metF gene or nucleotide sequences which code for it are enhanced;

b) concentration of the L-amino acid in the medium or in the cells of the bacteria, and

c) isolation of the L-amino acid.

10. The process as claimed in claim 9, wherein bacteria in which further genes of the biosynthesis pathway of the desired L-amino acid are additionally enhanced are employed.

11. The process as claimed in claim 9, wherein bacteria in which the metabolic pathways which reduce the formation of the desired L-amino acid are at least partly eliminated are employed.

12. The process as claimed in claim 9, wherein a strain transformed with a plasmid vector is employed, and the plasmid vector carries the nucleotide sequence which codes for the metF gene.

13. The process as claimed in claim 9, wherein the expression of the polynucleotide(s) which code(s) for the metF gene is enhanced, in particular over-expressed.

14. The process as claimed in claim 9, wherein the catalytic properties of the enzyme encoded by metF are increased.

15. The process as claimed in claim 9, wherein for the preparation of L-methionine, coryneform microorganisms have one or more enhanced genes selected from the group consisting of

15.1 the lysC gene which codes for a feed back resistant aspartate kinase,

15.2 the gap gene which codes for glycerolaldehyde 3-phosphate dehydrogenase,

15.3 the pgk gene which codes for 3-phosphoglycerate kinase,

15.4 the pyc gene which codes for pyruvate carboxylase,

15.5 the tpi gene which codes for triose phosphate isomerase,

15.6 the metA gene which codes for homoserine O-acetyltransferase,

15.7 the metB gene which codes for cystathionine gamma-synthase,

15.8 the aecD gene which codes for cystathionine gamma-lyase,

15.9 the glyA gene which codes for serine hydroxymethyltransferase,

15.10 the metY gene which codes for O-acetylhomoserine sulfhydrylase.

16. The process as claimed in claim 9, wherein for the preparation of L-methionine, the coryneform

microorganisms have one or more attenuated genes selected from the group consisting of

16.1 the thrB gene which codes for homoserine kinase,

16.2 the ilvA gene which codes for threonine dehydratase,

16.3 the thrC gene which codes for threonine synthase,

16.4 the ddh gene which codes for meso-diaminopimelate D-dehydrogenase,

16.5 the pck gene which codes for phosphoenol pyruvate carboxykinase,

16.6 the pgi gene which codes for glucose 6-phosphate isomerase,

16.7 the poxB gene which codes for pyruvate oxidase.

17. The process of claims 9, wherein microorganisms of the species Corynebacterium glutamicum are employed.

18. The process as claimed in claim 17, wherein the Corynebacterium glutamicum strain ATCC13032/pCREmetF is employed.

19. A process for preapring an L-methionine-containing animal feedstuffs additive, comprising:

a) culture and fermentation of an L-methionine-producing microorganism in a fermentation medium;

b) removal of water from the L-methionine-containing fermentation broth (concentration);

c) removal of an amount of 0 to 100 wt.% of the biomass formed during the fermentation; and

d) drying of the fermentation broth obtained according to b) and/or c) to obtain the animal feedstuffs additive in the desired powder or granule form.

20. The process as claimed in claim 19, wherein microorganisms are employed in which further genes of the biosynthesis pathway of L-methionine are additionally enhanced.

21. The process as claimed in claim 20, wherein microorganisms are employed in which the metabolic pathways which reduce the formation of L-methionine are at least partly eliminated.

22. The process as claimed in claim 20, wherein expression of the polynucleotide(s) which code(s) for the metF gene is enhanced.

23. The process of claim 19, wherein microorganisms of the species Corynebacterium glutamicum are employed.

24. The process as claimed in claim 23, wherein the Corynebacterium glutamicum strain ATCC13032/pCREmetF is employed.

25. The process as claimed in claimed claim 19, wherein one or more of the following steps are additionally carried out:

e) addition of one or more organic substances, including L-methionine and/or D-methionine and/or the racemic mixture D,L-methionine, to the products obtained according to b), c) and/or d);

f) addition of auxiliary substances selected from the group consisting of silicas, silicates, stearates, grits and bran to the substances obtained according to b) to e) for stabilization and to increase storability; or

g) conversion of the substances obtained according to b) to f) into a form stable in rumen, by coating them with film-forming agents.

26. The process as claimed in claim 19 or 25, wherein a portion of the biomass is removed.

27. A process as claimed in claim 26, wherein essentially 100% of the biomass is removed.

28. The process as claimed in claim 19 or 25, wherein the water content is up to 5 wt.%.

29. The process as claimed in claim 28, wherein the water content is less than 2 wt.%.

30. The process as claimed in claim 25, wherein the film-forming agents are metal carbonates, silicas, silicates, alginates, stearates, starches, gums or cellulose ethers.

31. An animal feedstuffs additive prepared as claimed in claim 19.

32. An animal feedstuffs additive as claimed in claim 31, which comprises 1 wt.% to 80 wt.% L-methionine, D-methionine, D,L-methionine or a mixture thereof, based on the dry weight of the animal feedstuffs additive.

33. A process for obtaining RNA, cDNA or DNA in order to isolate nucleic acids, or polynucleotides or genes which code for methylene tetrahydrofolate reductase or have a high similarity to the sequence of the methylene tetrahydrofolate reductase gene, which comprises employing the polynucleotide sequences as claimed in claim 1 as hybridization probes.